We claim:

1. A substantially purified nucleic acid molecule that encodes a maize or soybean enzyme or fragment thereof, wherein said maize or soybean enzyme is selected from the group consisting of:

(a) methionine adenosyltransferase,

(b) S-adenosyl-methionine decarboxylase,

(c) aspartate kinase,

(d) aspartate-semialdehyde dehydrogenase,

(e) cystathionine gamma-synthase,

(f) cystathionine beta-lysase, and

(g) 5-methyltetrahydropteroyltriglutamate-homocysteine-S-methyltransferase.

2. The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 3204.

3. A substantially purified maize or soybean enzyme or fragment thereof, wherein said maize or soybean enzyme is selected from the group consisting of

(a) methionine adenosyltransferase or fragment thereof;

(b) S-adenosyl-methionine decarboxylase or fragment thereof;

(c) aspartate kinase or fragment thereof;

(d) aspartate-semialdehyde dehydrogenase or fragment thereof;

(e) cystathionine gamma-synthase or fragment thereof;

(f) cystathionine beta-lysase or fragment thereof; and

(g) 5-methyltetrahydropteroyltriglutamate-homocysteine-S-methyltransferase or fragment thereof.

4. A substantially purified maize or soybean enzyme or fragment thereof according to claim 3, wherein said maize or soybean enzyme or fragment thereof is encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of consisting of SEQ ID NO: 1 through SEQ ID NO: 3204.

5. A substantially purified antibody or fragment thereof which is capable of specifically binding to a specific maize or soybean enzyme or fragment thereof according to claim 4.

6. A transformed plant having a nucleic acid molecule which comprises:

(A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule;

(B) a structural nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of

(a) a nucleic acid sequence which encodes for methionine adenosyltransferase or fragment thereof;

(b) a nucleic acid sequence which encodes for S-adenosyl-methionine decarboxylase or fragment thereof;

(c) a nucleic acid sequence which encodes for aspartate kinase or fragment thereof;

(d) a nucleic acid sequence which encodes for aspartate-semialdehyde dehydrogenase or fragment thereof;

(e) a nucleic acid sequence which encodes for cystathionine gamma-synthase or a fragment thereof;

(f) a nucleic acid sequence which encodes for cystathionine beta-lysase or a fragment thereof;

(g) a nucleic acid sequence which encodes for 5-methyltetrahydropteroyl-triglutamate-homocysteine-S-methyltransferase or a fragment thereof; and

(h) a nucleic acid sequence which is complementary to any of the nucleic acid sequences of (a) through (g); and

(C) a 3' non-translated sequence that functions in said plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of said mRNA molecule.

7. The transformed plant according to claim 5, wherein said structural gene is complementary to any of the nucleic acid sequences of (a) through (g).

8. A method for determining a level or pattern in a plant cell of an enzyme in a plant metabolic pathway comprising:

(A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, said marker nucleic acid molecule selected from the group of marker nucleic acid molecules which specifically hybridize to a nucleic acid molecule having the nucleic acid sequence of SEQ ID NO: 1 through SEQ ID NO: 3204 or compliments thereof, with a complementary nucleic acid molecule obtained from said plant cell or plant tissue, wherein nucleic acid hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said plant cell or plant tissue permits the detection of an mRNA for said enzyme;

(B) permitting hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said plant cell or plant tissue; and

(C) detecting the level or pattern of said complementary nucleic acid, wherein the detection of said complementary nucleic acid is predictive of the level or pattern of said enzyme in said plant metabolic pathway.

9. The method of claim 8, wherein said level or pattern is detected by *in situ* hybridization.

10. A method of determining a mutation in a plant whose presence is predictive of a mutation affecting a level or pattern of a protein comprising the steps:

(A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid, said marker nucleic acid selected from the group of marker nucleic acid molecules which specifically hybridize to a nucleic acid molecule having a nucleic acid sequence selected from the group of SEQ ID NO: 1 through SEQ ID NO: 3204 or complements thereof and a complementary nucleic acid molecule obtained from said plant, wherein nucleic acid hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said plant permits the detection of a polymorphism whose presence is predictive of a mutation affecting said level or pattern of said plant methionine pathway enzyme in said plant;

(B) permitting hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said plant; and

(C) detecting the presence of said polymorphism, wherein the detection of said polymorphism is predictive of said mutation.

11. A method of producing a plant containing an overexpressed protein comprising:

(A) transforming said plant with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a promoter region, wherein said promoter region is linked to a structural region, wherein said structural region has a nucleic acid sequence selected from group consisting of SEQ ID NO: 1 through SEQ ID NO: 3204 wherein said structural region is linked to a 3' non-translated sequence that functions in the plant to cause termination of

transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and wherein said functional nucleic acid molecule results in overexpression of the protein; and

(B) growing said transformed plant.